

Complete mitochondrial genome of the olive weevil, *Dyscerus cribripennis* (Coleoptera: Curculionidae)

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ABSTRACT

The olive weevil *Dyscerus cribripennis* (Coleoptera: Curculionidae) is an uncontrollable noxious insect to *Olea europaea*. The 15,977 bp complete mitochondrial genome of *D. cribripennis* contained 13 protein-coding genes (PCGs), 2 ribosomal RNA genes (rRNAs), 21 transfer RNA genes (tRNAs), and a control region (GenBank accession number MW023069). The *trnI* was not found in the *D. cribripennis* mitogenome. The phylogenetic analysis based on mitogenomes showed that *D. cribripennis* is closed related with *Hylobitelus xiaoi*.

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KEYWORDS

Olive weevil; *Dyscerus cribripennis*; mitochondrial genome; phylogenetic analysis

The olive weevil, *Dyscerus cribripennis* Matsumura et Kono (Coleoptera: Curculionidae) is an uncontrollable pest which caused serious damage to *Olea europaea* (Gao et al. 2018; Xiao 2020). The larvae of *D. cribripennis* bore into the stem base of bole and the imagoes gnaw at shoots. Adult specimens of *D. cribripennis* were collected from Lizhou District, Guangyuan City, Sichuan Province, China (N32°23'20", E105°39'32") in 18 November 2019. The specimen was deposited in the insect specimen room of College of

Forestry, Sichuan Agricultural University (voucher no. D018003.2).

The circular mitochondrial genome of *D. cribripennis* was 15,977 bp in length (GenBank accession number MW023069). This mitogenome contained 13 protein-coding genes (PCGs), 2 ribosomal RNA genes (rRNAs), 21 transfer RNA genes (tRNAs), and a control region. The *trnI* was not found in the *D. cribripennis* mitogenome, as observed in *Sympiezomias velatus* (Tang et al. 2017). The gene order and orientation of

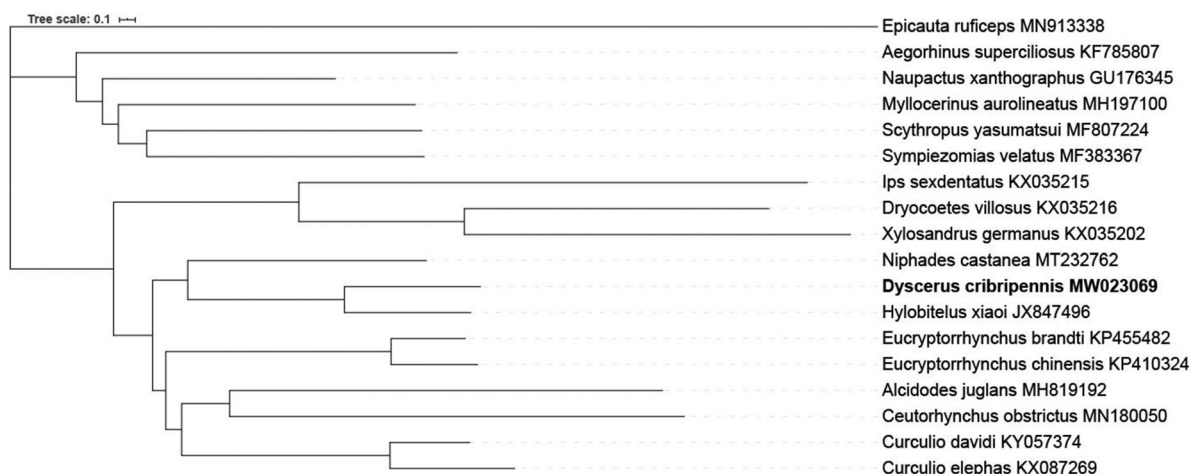


Figure 1. Bayesian Inference phylogenies were inferred using MrBayes 3.2.6 under partition model (2 parallel runs, 2,000,000 generations), in which the initial 25% of sampled data were discarded as burn-in. Bootstrap values were indicated around nodes. GeneBank accession numbers of each species were listed in the tree.

D. cribripennis are identical to the inferred ancestral arrangement of insects (Boore 1999).

The nucleotide composition of the mitogenome was significantly biased (A, G, C, and T was 39.18%, 9.33%, 15.17%, and 36.31%, respectively), with A + T contents of 75.49%. The AT-skew and GC-skew of this genome were 0.038 and -0.238 , respectively. Fourteen genes were transcribed on the J-strand, whereas the others were oriented on the N-strand. Gene overlaps were present at 12 gene junctions and involved a total of 94 bp, and the longest overlap (41 bp) existed between *trnH* and *nad4*.

The phylogenetic tree (Zhang et al. 2020) were constructed based on the amino acid sequences of the 13 PCGs from the mitochondrial genomes of 17 Curculionidae species, and *Epicauta ruficeps* was used as an outgroup. The result supported that *D. cribripennis* is closed related with *Hylobitelus xiaoi* (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the author(s).

Date availability statement

The data that support the findings of this study are openly available in the NCBI Genbank database at <https://www.ncbi.nlm.nih.gov/genbank/>, reference number MW023069.

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